

Sequence Listing

<110> Lee, James
Wood, William I.

<120> VEGF-RELATED PROTEIN

<130> P0963R1D1

<140> US 09/313,299

<141> 1999-05-17

<150> US 08/706,054

<151> 1996-08-30

<150> US 60/003,491

<151> 1995-09-08

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<211> 2031

<212> DNA

<213> artificial sequence

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<213> artificial sequence

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 <212> PRT
 <213> artificial sequence

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 35 40 45
 30 Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu
 50 55 60
 Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro
 65 70 75
 35 Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp
 80 85 90
 Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu
 95 100 105
 40 Thr Ile Lys Phe Ala Ala Ala His Thr Asn Thr Glu Ile Leu Lys
 110 115 120
 Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
 45 125 130 135
 Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr
 140 145 150
 50 Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys
 155 160 165
 Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr
 55 170 175 180
 Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly
 185 190 195
 60 Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg
 200 205 210

	Cys Met Ser Lys	Leu Asp Val Tyr Arg	Gln Val His Ser Ile	Ile
		215	220	225
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		230	235	240
	Lys Thr Cys Pro	Thr Asn Tyr Met Trp	Asn Asn His Ile Cys	Arg
		245	250	255
10	Cys Leu Ala Gln	Glu Asp Phe Met Phe	Ser Ser Asp Ala Gly	Asp
		260	265	270
	Asp Ser Thr Asp	Gly Phe His Asp Ile	Cys Gly Pro Asn Lys	Glu
		275	280	285
15	Leu Asp Glu Glu	Thr Cys Gln Cys Val	Cys Arg Ala Gly Leu	Arg
		290	295	300
	Pro Ala Ser Cys	Gly Pro His Lys Glu	Leu Asp Arg Asn Ser	Cys
20		305	310	315
	Gln Cys Val Cys	Lys Asn Lys Leu Phe	Pro Ser Gln Cys Gly	Ala
		320	325	330
25	Asn Arg Glu Phe	Asp Glu Asn Thr Cys	Gln Cys Val Cys Lys	Arg
		335	340	345
	Thr Cys Pro Arg	Asn Gln Pro Leu Asn	Pro Gly Lys Cys Ala	Cys
		350	355	360
30	Glu Cys Thr Glu	Ser Pro Gln Lys Cys	Leu Leu Lys Gly Lys	Lys
		365	370	375
	Phe His His Gln	Thr Cys Ser Cys Tyr	Arg Arg Pro Cys Thr	Asn
35		380	385	390
	Arg Gln Lys Ala	Cys Glu Pro Gly Phe	Ser Tyr Ser Glu Glu	Val
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		20	25	30
55	Glu Gly Gly Gly	Gln Asn His His Glu	Val Val Lys Phe Met	Asp
		35	40	45
	Val Tyr Gln Arg	Ser Tyr Cys His Pro	Ile Glu Thr Leu Val	Asp
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60	Ile Phe Gln Glu	Tyr Pro Asp Glu Ile	Glu Tyr Ile Phe Lys	Pro

5 Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
 80 85 90
 Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln
 95 100 105
 10 Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met
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<211> 149

20 <212> PRT

<213> artificial sequence

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 35 40 45
 Val Trp Gly Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp
 50 55 60
 35 Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro
 65 70 75
 40 Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu
 80 85 90
 Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Gln
 95 100 105
 45 Leu Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu
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<211> 8

<212> PRT

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1				5			8

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<211> 9

<212> PRT

<213> artificial sequence

<400> 10

Ser	Leu	Arg	Arg	Arg	Gln	Gln	Gln	Asp
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<213> artificial sequence

<400> 11

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5 <210> 12
<211> 13
<212> PRT
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10 <400> 12
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Sequence Listing

<110> Lee, James
Wood, William I.

<120> VEGF-RELATED PROTEIN

<130> P0963R1D1

<140> US 09/313,299

<141> 1999-05-17

<150> US 08/706,054

<151> 1996-08-30

<150> US 60/003,491

<151> 1995-09-08

<160> 12

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<211> 2031

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<221> Human

<222> 1-2031

<223> Sequence source: VRP

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 <212> DNA
 <213> Human

<220>
 <221> Human
 <222> 1-2031
 <223> Sequence source: complement to SEQ ID NO. 1
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<210> 3
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<220>
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 <222> 1-419
 <223> Sequence source: VRP

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 50 55 60
 Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro
 65 70 75
 Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp
 80 85 90
 Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu
 95 100 105
 Thr Ile Lys Phe Ala Ala Ala His Thr Asn Thr Glu Ile Leu Lys
 110 115 120
 Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
 125 130 135
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 140 145 150
 Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys

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Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly	185		190		195
Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	200		205		210
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile	215		220		225
Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn	230		235		240
Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg	245		250		255
Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp	260		265		270
Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu	275		280		285
Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg	290		295		300
Pro Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys	305		310		315
Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala	320		325		330
Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg	335		340		345
Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys	350		355		360
Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys	365		370		375
Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr Asn	380		385		390
Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser Glu Glu Val	395		400		405
Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met Ser	410		415		419

<210> 4
 <211> 147
 <212> PRT
 <213> Human

<220>
 <221> Human
 <222> 1-147
 <223> Sequence source: VEGE-121

<400> 4

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	
1				5					10					15	
Leu	Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	
				20					25					30	
Glu	Gly	Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	
				35					40					45	
Val	Tyr	Gln	Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	
				50					55					60	
Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	
				65					70					75	
Ser	Cys	Val	Pro	Leu	Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	
				80					85					90	
Gly	Leu	Glu	Cys	Val	Pro	Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	
				95					100					105	
Ile	Met	Arg	Ile	Lys	Pro	His	Gln	Gly	Gln	His	Ile	Gly	Glu	Met	
				110					115					120	
Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Asp	
				125					130					135	
Arg	Ala	Arg	Gln	Glu	Lys	Cys	Asp	Lys	Pro	Arg	Arg				
				140					145		147				

<210> 5

<211> 149

<212> PRT

<213> Human

<220>

<221> Human

<222> 1-149

<223> Sequence source: PIGE-131

<400> 5

Met	Pro	Val	Met	Arg	Leu	Phe	Pro	Cys	Phe	Leu	Gln	Leu	Leu	Ala	
1				5					10					15	
Gly	Leu	Ala	Leu	Pro	Ala	Val	Pro	Pro	Gln	Gln	Trp	Ala	Leu	Ser	
				20					25					30	
Ala	Gly	Asn	Gly	Ser	Ser	Glu	Val	Glu	Val	Val	Pro	Phe	Gln	Glu	
				35					40					45	
Val	Trp	Gly	Arg	Ser	Tyr	Cys	Arg	Ala	Leu	Glu	Arg	Leu	Val	Asp	
				50					55					60	
Val	Val	Ser	Glu	Tyr	Pro	Ser	Glu	Val	Glu	His	Met	Phe	Ser	Pro	
				65					70					75	
Ser	Cys	Val	Ser	Leu	Leu	Arg	Cys	Thr	Gly	Cys	Cys	Gly	Asp	Glu	
				80					85					90	
Asn	Leu	His	Cys	Val	Pro	Val	Glu	Thr	Ala	Asn	Val	Thr	Met	Gln	

	95	100	105
Leu Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu			
	110	115	120
Thr Phe Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu			
	125	130	135
Lys Met Lys Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg			
	140	145	149

<210> 6
 <211> 299
 <212> DNA
 <213> Unknown

<220>
 <223> Sequence source: EST

<220>
 <221> unsure
 <222> 74
 <223> unknown base

<400> 6
 ccgtctacag atgtgggggt tgctgcaata gtgaggggct gcagtgcattg 50
 aacaccagca cgagctacct cagnaagacg ttatttgaaa ttacagtgcc 100
 tctctctcaa ggccccaac cagtaacaat cagttttgcc aatcacactt 150
 cctgccgatg catgtctaaa ctggatgttt acagacaagt tcattccatt 200
 attagacgtt ccctgccagc aactactacca cagtgtcagg cagcgaacaa 250
 gacctgcccc accaattaca tgtggaataa tcacatctgc agatgcctg 299

<210> 7
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Sequence source: synthetic probe

<400> 7
 ctggtgttca tgcactgcag cccctcacta ttgcagcaac ccccatctt 50

<210> 8
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Sequence source: synthetic probe

<400> 8
 gcatctgcag atgtgattat tccacatgta attggtgggg caggtcttgt 50

<210> 9
 <211> 8
 <212> PRT

<213> Human

<220>

<221> Human

<222> 1-8

<223> Sequence source: Flt4 partial sequence

<400> 9

Tyr Ser Met Thr Pro Pro Thr Leu
1 5 8

<210> 10

<211> 9

<212> PRT

<213> Human

<220>

<221> Human

<222> 1-9

<223> Sequence source: Flt4 partial sequence

<400> 10

Ser Leu Arg Arg Arg Gln Gln Gln Asp
1 5 9

<210> 11

<211> 40

<212> PRT

<213> Unknown

<220>

<223> Sequence source: Herpes glycoprotein D partial sequence

<400> 11

Lys Tyr Ala Leu Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn
1 5 10 15

Arg Phe Arg Gly Lys Asp Leu Pro Val Leu Asp Gln Leu Leu Glu
20 25 30

Gly Gly Ala Ala His Tyr Ala Leu Leu Pro
35 40

<210> 12

<211> 13

<212> PRT

<213> Human

<220>

<221> Human

<222> 1-13

<223> Sequence source: partial VRP sequence

<400> 12

Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe Glu
1 5 10 13



45
100

Application No.: _____

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: *Diskette submitted was blank.*

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

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For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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